

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 27, 2001, 17:07:35 ; Search time 2462.53 Seconds

(without alignments)
2690.912 Million cell updates/sec

Title: US-09-784-340-3_COPY_7800_8500

Perfect score: 701
Sequence: 1 ggtgtggtcgaactgagagaaaa.....taggattccagaaaaaatra 701

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*
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257: gb_est188:*
258: gb_est189:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Db 8 ACBA 5

RESULT 2
LOCUS AQ319346 667 bp DNA GSS 06-MAY-1999
DEFINITION RPII11-99P4.TV RPII-11 Homo sapiens genomic clone RPII-11-99P4, DNA sequence.
ACCESSION AQ319346
VERSION AQ319346.1 GI:4052311
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 667)
AUTHORS Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
TITLE Use of human BAC End Sequences for Sequence-Ready Map Building
JOURNAL Unpublished (1998)
COMMENT Other GSSs: RPII11-99P4.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeetigr.org
Clones are derived from the human BAC library RPII-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="GDB:753795"
/db_xref="taxon:9606"
/clone="RPII-11-99P4"
/clone.lib="RPII-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI; RPII11 Human Male BAC Library"

BASE COUNT 152 a 181 c 118 g 216 t

Query Match 19.9%; Score 139.4; DB 227; Length 667;
Best Local Similarity 59.9%; Pred. No. 1.1e-25;
Matches 348; Conservative 0; Mismatches 211; Indels 22; Gaps 6;

QY 1 ggtgtgtcagtgagaaacatgagaaactaaccacaacataaataaagaac 60
|||||
Db 583 GTGTCTCTAAATGAGAAACGAGAGACACACTAACAATAATGAAAAAGC 524
|||||
QY 61 agtct-tcttgaccattctagaagaaagagttcagatccctgtlaaggccataga 119
|||||
Db 523 ATTGTATTACTTACAGATCCAGAGGAGAGAGCAGACACCTCACAGGCCAACAGA 464
|||||
QY 120 agagaataattctctgggaaagacatccaacatgaaatgagagaccagaagaagt 179
|||||
Db 463 AGGGAAGAGACTCTGTGACATGTATGCTCAACCGCAGGTGGGATCCAAAGAGAGAAG 404
|||||
QY 180 gagagatcta-----gtgtccaaatgttaactgagatccaggtgttacccagg 229
|||||
Db 403 GAGGAGAGAGAGATGAGACCTGTGGGCCACACTTTACTGCATTTTAAAGCATTTCCCAAG 344
|||||
QY 230 tgggtttccaatggggaactgtaattgtaagtttaatgcaagcaggcaaaagtcata 289

Db 343 TAGATTTCTCGAGGAGAGTTCTAATTTGTAAGTATGAGCAAGCAGACAAAGTTCCATG 284
|||||
QY 290 gaggcattctgagactggaagat-----agtcacttgcatactgcacagaactctg 342
|||||
Db 283 GATCCATGCTGTGACTAAGAGAGTCACTGGGTGTATCTGTGGTAGTCATTTGAGGATGGG 224
|||||
QY 343 atccatgattcaagcccaagtagctgtatctagttgc--ctataagggtgtaccagg 400
|||||
Db 223 GTCACTGGGGCAAG-TCAAGTGGTGTATCTTGTCTGTCCACACAGAGGTGTCTACACAGA 165
|||||
QY 401 aggcagtggtgaagaaatccctgactgacacacatlgagaaatgagagaggtggaag 460
|||||
Db 164 TCATGTCTGTATAGGTAATATATTCAGATGAGCACCATGAGCAGACAGAGAGAGA 105
|||||
QY 461 atttaaacggtgtgagtggttactaagaacctgtctgtggttg--gaaatcacctat 519
|||||
Db 104 ACTGGAACGTGTGTAAGGGTGTACTAAGCCCTCTGTGGTAGGAAAGTCCAAATTCAT 45
|||||
QY 520 atttaaatgcatagccagacacataaataatgaagt 560
|||||
Db 44 ATTCAAAATGATGTTGTAGGCAATATATAATATGAGAA 4

RESULT 3
LOCUS B46805 397 bp DNA GSS 21-OCT-1997
DEFINITION HS-1066-A1-C09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 270 Col-17 Row-E, DNA sequence.
ACCESSION B46805
VERSION B46805.1 GI:2551639
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 397)
AUTHORS Mahairas, G.G., Zackrone, K.D., Smith, T., Tipton, S., Schmidt, S., Traicoff, R., Abajian, C., Blanchard, A., West, A. and Hood, L.E.
TITLE Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence Tagged Connectors
JOURNAL Unpublished (1997)
COMMENT Contact: Mahairas Gg, Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Email: kzackrone@u.washington.edu
Sequence Tagged Connector
Plate: CT 270 row: E column: 17
Class: BAC ends
High quality sequence stop: 397.

FEATURES
source Location/Qualifiers
1..397
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-CT 270 Col-17 Row=E"
/clone.lib="CIT Human Genomic Sperm Library C"
/sex="M"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 113 a 65 c 108 g 111 t

Query Match 19.8%; Score 138.6; DB 256; Length 397;
Best Local Similarity 67.4%; Pred. No. 1.5e-25;
Matches 242; Conservative 0; Mismatches 109; Indels 8; Gaps 3;

QY 217 ggtgtaccagtggtgtgttccaatggggaactgtaattgaggtttaaagcagg 276
|||||
Db 26 GGTATCATCTAGTGGGTCTCCCATTTGGCAATTTCTACTGTGGATTTACGACAGACTGG 85

QY	277	cataaagtcacatgagagcgatcttcgagacgtgaagaatagtcacttggcatatctgca--c 334
Db	86	ATCACAATCTCATGCGATCAACACATGTGCTAAAGAGTGCGTGTGGCTTATCGCATG 145
QY	335	agaactgcatcacttgatttccaagcccaagttagcgctgatactgaattgctcttaagggtgct 394
Db	146	TGCTATTTAGGAGAGTGGAGGCGCATTTAGTATGTTGTATCTTAAGCTGTCTCATAGGGCAATG 205
QY	395	accagaaggcagctgtgtaagtaa----aaatccctgactgaacacatltgagaatlgaa 449
Db	206	GTCACTAGGAAGAGGTGTTATATATAGGAGACATCTGGATTCATCTTGAAGAACTGGGA 265
QY	450	ggaagtggaagaattttaaacygtgtaagtggttgaactaaagccctgcttctgltatg--ga 508
Db	266	GGAGCGAGAGAACTGGAAATTTGTGTAAAGGATATCTTAAGCCCTGCTACTATAGAGAAA 325
QY	509	attcaactatatttcaaatgcatagccagacacacataaataatataagaattcaccca 567
Db	326	GTTAATCTCATATTATTACATTCGATTCGTCGAGGCAACATTAACCTGTATAGATTTCACACA 384
RESULT	4	
LOCUS	AO264450/c	
DEFINITION	AO264450 678 bp DNA GSS 27-OCT-1998	
ACCESSION	CITBI-EL-2509C10.TF CITBI-EL Homo sapiens genomic clone 2509C10,	
VERSION	AO264450	
KEYWORDS	AO264450.1 GI:3792817	
SOURCE	GSS.	
ORGANISM	human.	
REFERENCE	Homo sapiens	
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 678) Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Grainger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.	
TITLE	Use of a random human BAC End Sequence Database for Sequence-Ready Map Building	
JOURNAL	Unpublished (1998)	
COMMENT	Other_GSS: CITBI-EL-2509C10.TF Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/ldb/humgen/bac_end_search/bac_end_search.html. Seq primer: M3-21 Class: BAC ends.	
FEATURES		
source	Location/Qualifiers	
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	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/clone="2509C10"	
	/clone_1lb="CITBI-EL"	
	/sex="male"	
	/cell_type="sperm"	
	/note="Vector: pBelOBAcl1; Site_1: EcoRI; Site_2: EcoRI; Caltech Human BAC Library D"	
BASE COUNT	163 a 184 c 117 g 214 t	
ORIGIN		
Query Match	19.6%; Score 137.4; DB 226; Length 678;	
Best Local Similarity	60.0%; Pred. No. 3.5e-25;	
Matches	326; Conservative 0; Mismatches 196; Indels 21; Gaps 5	
1	gtgttggtcgaatgtagaaacatgaggagaacttaaccaaacataaataacagaac 60	

[illegible]

	RESULT	7	A0506772/c	601 bp	DNA	GSS	-29-APR-1999
	LOCUS	RPC1-I1-293D14	.rv	RPCI-I1 Homo sapiens genomic clone RPCI-I1-293D14			
	DEFINITION		, DNA sequence.				
	ACCESSION	A0506772					
	VERSION	A0506772.1	GI:4711519				
	KEYWORDS	GSS.					
	SOURCE	human.					
	ORGANISM	Homo sapiens					
	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 601)					
	AUTHORS	Zhao,S., Adams,M.D., Niernan,W., Malek,J., de Jong,P. and Venter .J.C.					
	TITLE	Use of BAC End Sequences from Library RPCI-I1 for Sequence-Ready Map Building					
JOURNAL	Unpublished (1997) other.GSSE: RPCI-I1-293D14.tv						
COMMENT	Contact: Shaying Zhao, William Niernan, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel.: 301 838 0200 Fax: 301 838 0208 Email: hbe@tigr.org Clones are derived from the human BAC library RPCI-I1. For BAC library availability, please contact Pieter de Jong (pietere@jng.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html .						
FEATURES	Seq primer: SP6 Class: BAC ends.						
SOURCE	Location/Oualifiers 1..601 /organism="Homo sapliens" /db_xref="GDB:7612213" /db_xref="taxon:9606" /clone="RPCI-I1-293D14" /clone_1lb="RPCI-I1" /sex="Male" /cell_type="Lymphocytes" /note="Vector: pBacc3.6; Site.1: EcoRI; Site.2: EcoRI; RPlcII Human Male BAC Library"						
BASE COUNT	135 a 161 c 103 g 202 t						
ORIGIN							
Query Match	18.3%:	Score 128;	DB 229;	Length 601;			
Best Local Similarity	59.5%:	Pred. No. 9.3e-23;					
Matches 339;	Conservative 0;	Mismatches 200;	Indels 31;	Gaps 6;			
OY	14	gagaaacaatggagggaacttaaccaaaccaataaatagaagaacagtcttc--g	71	*			
Db	566	GAGCAGCAGAACAATAATTAATGAATGCATTGAATAAATAAGCAATCTTTTTCCT	507				
OY	72	acctattctaagaaaagaagtgcagcatcccttgttaaagccaactcggaagaagaatatc	131				
Db	506	TTAGATCCCAAAGAGAAAGGGCATCATGCCCTCACAGGGCGGTGGAAAAGMAAGTTA	447				
OY	132	tctggaaaaacacataaccaatgtaatggagaccaga-----agagtgtagg	183				
Db	446	TCTGGAACACCATTCTCAACCAGCTGGTGGAAGCAAGAAAAAGAGAGAGCAAGA	387				
OY	184	gatcatagtgccaaaagttaacttyggaatcggaaggltttactaagttygtttccaaty	243				
Db	386	GACCAAAAGATCCAAGCTTCATTGGTTTTCCAAAACATATACCAAGCAGGTTCCGAAG	327				
OY	244	ggaactgtaattgttgagttaatgbgcaagcgcgcgaagtcattcgagsgatcttgaga	303				
Db	326	AGAGCTCTTAACACTGGAATTTTAAACAAGTAGTTCAGATTCCAAAGATACACTGTCA	267				

[illegible]

FEATURES	Source
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 759) Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
TITLE	Contact: Shaying Zhao, William Nierman, Mark Adams
JOURNAL	Department of Eukaryotic Genomics
COMMENT	The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: hbe@tigr.org Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@jeong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html Seq primer: T7 Class: BAC ends.
RESULTS	Location/Qualifiers
1. 759	/organism="Homo sapiens"

			/db_xref="GDB:7541740"	
			/db_xref="taxon:9606"	
			/clone="RPC1-11-109L5"	
			/clone_id="RPC1-11"	
			/sex="Male"	
			/cell_type="Lymphocytes"	
			/note="Vector: PBAC3.6; Site: 1: EcoRI; site_2: EcoRI; RPC111 Human Male BAC Library"	

BASE COUNT	188 a	221 c	142 g	208 t
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ORIGIN	
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Query Match	17.6%; Score 123.2; DB 227; Length 759;
Best Local Similarity	54.4%; Pred. No. 1,7e-21;
Matches 294; Conservative	0; Mismatches 233; Indels 8; Gaps 2;

OY	18	aacatgaggaagaacttaccacaacataaaataacagaacagc-tctctttggacct	76
Db	533	AACACATGAGAGAAGACTCAACAACATGAATAACAGANISCATATTACTTACAGA	474
OY	77	tcttagagaaaagtgcagcatcccttgtaaggccaattgaaagaanaattctgtg	136
Db	473	TCCCGGGGAGAGAGAGCAGTGTCCTTCAAGGCCAGGCGAAGGAGGGAGGCATAGG	414
OY	137	gaaaagcacattcaaccaatgaatgagaaccaaagaagaagagtgtaagatcattgcca	196
Db	413	ACATATTATGCTCCATCAGCAGGTGGAGCACAGACAGACAGAACACACAGCTGGGAGCCA	354
OY	197	aatgttaactgagagtcacagagtggttacttagtggttttaaayggnaactglaattg	256
Db	353	AAGCCTTTACGGGGGTGCAGATTATCGCCCAAGTAAGTTTACATVGGGAAGTTGTAATTG	294
OY	257	gtaggtttaatgcaagcgacaaatgccatgtagaggaattctgagactgaagaatgac	316
Db	293	GTCGGTTTAGAGCAAAACAGGAGGAGTCCCCTGGGATTTATCTGCACCTAAGAGGGTTC	234
OY	317	acttgagatatctgcagaatctgcattgcattgatattaaucccagtagagctglatcag	376
Db	233	TCTGAAGCATACCTTGCAAGTCTGTGTGGGTGTGGGGTCAAGTGGATCAAGAAAG	174
OY	377	tgtgtcctaaggttggttacccagagggcagtggtgtaagtaaaaaactgcattgaacacat	436
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OY	437	tgaagaaatggaagagtggaagattttaaacygtgtcagtgltgtactaagacctgtc	496
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LOCUS	AO680752.c
DEFINITION	HS_5481_B1_F07_17A RPC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=1057 Col=L3 Row=L, DNA sequence.
ACCESSION	AO680752
VERSION	AO680752.1 GI:5229556
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SOURCE	Human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 522) Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE	99380589

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QY	210	aagcagcacaagaatccatctgagagcattctgactga...	atagtcactttgcatatc	329
Db	291	AAGCAGGAGATGATGTTCCAGAGAGTGGCAGACTGATGA...	TTGGGCCCTGTGGGCGATC	232
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Db	231	TGCACATTCCTAGGTGGGGGTGTAGAGGCTAGTGTGCCCA...	GGTTCTAGCTGTGCCATG	172
QY	388	gtgtgttaccagagagcagtggtgtt-----aagtaaaa...	tgactgaacacattgaga	442
Db	171	AGAAGTGTGTCACACAGAGAGTAGTGTATAGAGCAGATAT...	TGATCCACACATATAACA	112
QY	443	aatggaagagagtggaagattttaacaggtgtcagtggt...	taagacctgtcttgta	502
Db	111	ACTGGAGAACAGTGTGAGAACCCAGCACTTTGTCCGGGG...	TGAGCCCTGTGTTTGGTG	52
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DEFINITION	HS_3026_B1_D02.T7 CIT Approved Human			
ACCESSION	sapiens genomic clone Plate=3026 Col			
VERSION	AQ207718			
KEYWORDS	AQ207718.1 GI:3620453			
SOURCE	GSS.			
ORGANISM	human.			
REFERENCE	Homo sapiens			
AUTHORS	Eukaryota; Metazoa; Chordata; Crania			
	Mammalia; Eutheria; Primates; Catarrh			
	I (bsses 1 to 505)			
	Mahairas,G.G., Wallace,J.C., Smith,K.			
	Keller,A., Shaker,R., Furlong,J., Ye			
	Hood,L.			
TITLE	Sequence-tagged connectors: A sequen-			
	scanning the human genome			
JOURNAL	Proc. Natl. Acad. Sci. U. S. A. 96 (
MEDLINE	99380589			
COMMENT	Contact: Mahairas GG, Wallace JC, Ho-			
	High Throughput Sequencing Center			
	University of Washington			
	401 Queen Anne Avenue North, Seattle.			
	Tel: (206) 616-3618			
	Fax: (206) 616-3887			
	Email: jwallace@u.washington.edu			
	Sequence Tagged Connector			
	Plate: 3026 row: H column: 3			
	Class: BAC ends			
	High quality sequence stop: 505.			
FEATURES				
source	Location/Qualifiers			
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	/sex="male"			
	/note="Organ: sperm; Vector:			
	E-Coli DH10B"			
BASE COUNT	110 a 156 c 92 g 146 t			
ORIGIN				
Query Match	14.4%; Score 101.2;			
Best Local Similarity	59.5%; Pred. No. 7.7c			
Matches	286; Conservative 0; Mismatches			
QY	108	agccacatgagagaagaanaattctctgtgggaagaagc...	aacacatgatgagagacc	167
Db	495	AAGCCAGAGAGAAACGGGAGCTGTCTGGACACACACAC...	TACTTACTGAGTGAGAGC	436

